**Figure 1a**

**Variable Heavy Chain DNA**

**3076_VH1A** (SEQ ID NO: 1):
CAGGTGCAATTGGTTCAGTCTGGCGCGGAAGTGAAAAAACCGGGCAGCAGCGTGAAAGTGAGC
TGCAAAGCCTCCGGAGGCACTTTTTCTTCTAATGCTATTTCTTGGGTGCGCCAAGCCCCTGGGCA
GGGTCTCGAGTGGATGGGCAATATCTGGCCGATTTTTGGCACTGCGAATTACGCGCAGAAGTTT
CAGGGCCGGGTGACCATTACCGCGGATGAAAGCACCAGCACCGCGTATATGGAACTGAGCAGC
CTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTAATGGTTATCTTGATACTAATACTTA
TATTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3078_VH3** (SEQ ID NO: 2):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTGATTATGCTATGTCTTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCGCTATCCGTTATGATGGTAGCAATACCTATTATGCGGATAGCG
TGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGC
CTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTTATTATTCTGGTATTTATCAGCATAT
TGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3081_ VH3** (SEQ ID NO: 3):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTCTTCATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTCTATCTCTGGTCTTGGTAGCACTACCTATTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTTATCATTATGAGTATCATTATTTTTCTT
CTGGTTTTGATAATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3085_ VH1A** (SEQ ID NO: 4):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGC
TGCAAAGCCTCCGGATATACCTTTACTGGTTATTATATTAATTGGGTCCGCCAAGCCCCTGGGCA
GGGTCTCGAGTGGATGGGCTGGATCTTTCCGAATGGTGGCTCTACGGGTTACGCGCAGAAGTTT
CAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGC
CTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGGTAATATTTTTATTTTTGATTATTGG
GGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3086_VH3** (SEQ ID NO: 5):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTACTTCTTATTATATGCATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTATATCGATTCTTCTGGTAGCTCTACCTATTATGCGGATAGCGTG
AAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTCAGCTTATGCCTTTTGGTGGTTATTTTG
ATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3087_ VH3** (SEQ ID NO: 6):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGGTATCTCTGGTGATCCTAGCAATACCTATTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTT
GCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**Figure 1a (Continued)**

**3088_ VH3** (SEQ ID NO: 7):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCGGTATCTCTTCTTGGGGTAGCTCTACCTATTATGCGGATAGCG
TGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGC
CTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATT
ATTTTGCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3089_ VH2** (SEQ ID NO: 8):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTTCTGATGGTATGGGTGTGGGTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTCTTATCGATTGGGATGATGATAAGCGTTATAGCACCAGC
CTGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAA
CATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTTTTAATTGGTTTTATCGTCTTGCTT
TTGTTAATCCTGATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3101_ VH2** (SEQ ID NO: 9):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTACTTCTCGTGTTGGTGTGTCTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTCATATCGATTGGAATGATGATAAGTATTATAGCACCAGC
CTGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAA
CATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTGAGGATCGTCTTCTTGGTGGTTAT
GGTTATGATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3102_ VH4** (SEQ ID NO: 10):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACC
TGCACCGTTTCCGGAGGCAGCATTTCTGGTAATTATTGGTCTTGGATTCGCCAGGCCCCTGGGA
AGGGTCTCGAGTGGATTGGCGATTATCATGGCTCTACCTATTATAATCCGAGCCTGAAAGGCCG
GGTGACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGGCG
GAAGATACGGCCGTGTATTATTGCGCGCGTGAGCAGTATCATTGGGGTCTTGCTTGGACTGGTT
TTGATAATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3127_ VH5** (SEQ ID NO: 11):
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGAAAGCCTGAAAATTAGCT
GCAAAGGTTCCGGATATTCCTTTTCTACTTCTTGGGTTGGTTGGGTGCGCCAGATGCCTGGGAA
GGGTCTCGAGTGGATGGGCATTATCGATCCGGATATTAGCTATACCTCTTATTCTCCGAGCTTTC
AGGGCCAGGTGACCATTAGCGCGGATAAAAGCATTAGCACCGCGTATCTTCAATGGAGCAGCCT
GAAAGCGAGCGATACGGCCATGTATTATTGCGCGCGTTATCTTATGGGTCTTGGTTATGATGTTT
GGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3128_ VH2** (SEQ ID NO: 12):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTTCTTCTGGTATGTCTGTGTCTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTCGTATCTATTCTGATGATTCTAAGTCTTATAGCACCAGCC
TGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAAC
ATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTGCTGCTCATTGGAATGGTCCTCTTT
TTGATGTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**Figure 1a (Continued)**

**3129_ VH3** (SEQ ID NO: 13):
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTAATTATTCTATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTATATCTATGGTGGTGGTAGCTATACCTATTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTCAGGCTGGTATGTATTTTGATGTTTG
GGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3130_ VH4** (SEQ ID NO: 14):
CAGGTGCAATTGCAAGAAAGTGGTCCGGGCCTGGTGAAACCGGGCGAAACCCTGAGCCTGACC
TGCACCGTTTCCGGAGGCAGCATTGGTTATTATTGGAATTGGATTCGCCAGGCCCCTGGGAAGG
GTCTCGAGTGGATTGGCCATATCTCTCGTTTTGGCTCTACCAATTATAATCCGAGCCTGAAAGGC
CGGGTGACCATTAGCGTTGATACTTCGAAAAACCAGTTTAGCCTGAAACTGAGCAGCGTGACGG
CGGAAGATACGGCCGTGTATTATTGCGCGCGGGAGTATACTGGTAATGATTGGTATCGTCAGCA
GGGTCAGCATGCTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3131_ VH2** (SEQ ID NO: 15):
CAGGTGCAATTGAAAGAAAGCGGCCCGGCCCTGGTGAAACCGACCCAAACCCTGACCCTGACC
TGTACCTTTTCCGGATTTAGCCTGTCTAATTCTGGTGTTGGTGTGGGTTGGATTCGCCAGCCGCC
TGGGAAAGCCCTCGAGTGGCTGGCTGATATCTATTCTGATACTACTAAGCGTTATAGCACCAGCC
TGAAAACGCGTCTGACCATTAGCAAAGATACTTCGAAAAATCAGGTGGTGCTGACTATGACCAAC
ATGGACCCGGTGGATACGGCCACCTATTATTGCGCGCGTTATGGTGAGGCTTATTTTGATTATTG
GGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6183_VH3** (SEQ ID NO: 77)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGGTATTAATATGGAGTCTACTCGTATTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6184_VH3** (SEQ ID NO: 78)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTCATGATGGTAATGTTAAGTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6185_VH3** (SEQ ID NO: 79)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTATGAATGGTGATTATATTTCTTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**Figure 1a (Continued)**

**6186_VH3** (SEQ ID NO: 80)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTAATCTTTCTGGTTCTGCTAAGTATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6187_VH3** (SEQ ID NO: 81)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTTCTAATGGTGATATTACTTATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6188_VH3** (SEQ ID NO: 82)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTACTAATGGTTGGCAGACTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6189_VH3** (SEQ ID NO: 83)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTAATATGATTGGTAATGTTACTAATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6190_VH3** (SEQ ID NO: 84)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCTATATTAATCCTAATGGTATGATGACTAATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6192_VH3** (SEQ ID NO: 85)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGTTATTTCTCCTGGTGGTGAGGCTAAGTCTTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**Figure 1a (Continued)**

**6195_VH3** (SEQ ID NO: 86)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTGGTAATGGTGGTCATACTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6197_VH3** (SEQ ID NO: 87)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTATGGATGGTGTTTATAAGTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6200_VH3** (SEQ ID NO: 88)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTAATAATGGTAATGTTACTTATTATGCTGATTCTGTTA
AGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTG
CGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTGC
TTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6201_VH3** (SEQ ID NO: 89)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATTATATGAATTGGGTGCGCCAAGCCCCTGGGA
AGGGTCTCGAGTGGGTGAGCGCTATTTCTATGCATGGTGATACTACTTATTATGCTGATTCTGTT
AAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCT
GCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGATCTTCCTCTTGTTTATACTGGTTTTG
CTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6204_VH3** (SEQ ID NO: 90)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCCATATTCGTAAGAAGAATACTTCTTATACTACTGAGTATGCTGC
TTCTGTTAAGGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAA
CAGCCTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACT
GATTATTTTGCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**6214_VH3** (SEQ ID NO: 91)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGCTATGAATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCAATATTCAGCGTGTTGGTTCTACTTATTATGCTGATTCTGTTAA
GGGTCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCCTGC
GTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTGAGGATGGTTCTTATATGACTGATTATTTT
GCTTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**Figure 1a (Continued)**

**3077_VH1B** (SEQ ID NO: 111)
CAGGTGCAATTGGTTCAGAGCGGCGCGGAAGTGAAAAAACCGGGCGCGAGCGTGAAAGTGAGC
TGCAAAGCCTCCGGATATACCTTTACTTCTTATTCTATTAATTGGGTCCGCCAAGCCCCTGGGCA
GGGTCTCGAGTGGATGGGCTATATCGATCCGAATCGTGGCAATACGAATTACGCGCAGAAGTTT
CAGGGCCGGGTGACCATGACCCGTGATACCAGCATTAGCACCGCGTATATGGAACTGAGCAGC
CTGCGTAGCGAAGATACGGCCGTGTATTATTGCGCGCGTGAGTATATTTATTTTATTCATGGTAT
GCTTGATTTTTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3079_VH3** (SEQ ID NO: 112)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTAATTATGGTATGCATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCAATATCCGTTCTGATGGTAGCTGGACCTATTATGCGGATAGCG
TGAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGC
CTGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTCGTTATTGGTCTAAGTCTCATGCTTC
TGTTACTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**3080_ VH3** (SEQ ID NO: 113)
CAGGTGCAATTGGTGGAAAGCGGCGGCGGCCTGGTGCAACCGGGCGGCAGCCTGCGTCTGAG
CTGCGCGGCCTCCGGATTTACCTTTTCTTCTTATGGTATGCATTGGGTGCGCCAAGCCCCTGGG
AAGGGTCTCGAGTGGGTGAGCAATATCTATTCTGATGGTAGCAATACCTTTTATGCGGATAGCGT
GAAAGGCCGTTTTACCATTTCACGTGATAATTCGAAAAACACCCTGTATCTGCAAATGAACAGCC
TGCGTGCGGAAGATACGGCCGTGTATTATTGCGCGCGTAATATGTATCGTTGGCCTTTTCATTAT
TTTTTTGATTATTGGGGCCAAGGCACCCTGGTGACGGTTAGCTCA

**Figure 1b**

**Variable Heavy Chain Peptide**

(CDR Regions in **Bold** or underlined)

**3076_VH1A** (SEQ ID NO: 16):
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSNAIS**WVRQAPGQGLEWMG**NIWPIFGTANYAQKFQ**
**G**RVTITADESTSTAYMELSSLRSEDTAVYYCAR**NGYLDTNTYIDY**WGQGTLVTVSS

**3078_VH3** (SEQ ID NO: 17):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSDYAMS**WVRQAPGKGLEWVS**AIRYDGSNTYYADSVK**
**G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YYSGIYQHIDY**WGQGTLVTVSS

**3081_ VH3** (SEQ ID NO: 18):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYALH**WVRQAPGKGLEWVS**SISGLGSTTYYADSVK**
**G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**YHYEYHYFSSGFDN**WGQGTLVTVSS

**3085_ VH1A** (SEQ ID NO: 19):
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTGYYIN**WVRQAPGQGLEWMG**WIFPNGGSTGYAQKF**
**QG**RVTMTRDTSISTAYMELSSLRSEDTAVYYCAR**GNIFIFDY**WGQGTLVTVSS

**3086_VH3** (SEQ ID NO: 20):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFTSYYMH**WVRQAPGKGLEWVS**YIDSSGSSTYYADSVK**
**G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QLMPFGGYFDV**WGQGTLVTVSS

**3087_ VH3** (SEQ ID NO: 21):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYYMN**WVRQAPGKGLEWVS**GISGDPSNTYYADSVK**
**G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**DLPLVYTGFAY**WGQGTLVTVSS

**3088_ VH3** (SEQ ID NO: 22):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYAMN**WVRQAPGKGLEWVS**GISSWGSSTYYADSV**
**KG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**EDGSYMTDYFAY**WGQGTLVTVSS

**3089_ VH2** (SEQ ID NO: 23):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSSDGMGVG**WIRQPPGKALEWLA**LIDWDDDKRYSTSLK**
**T**RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**FNWFYRLAFVNPDV**WGQGTLVTVSS

**3101_ VH2** (SEQ ID NO: 24):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSRVGVS**WIRQPPGKALEWLA**HIDWNDDKYYSTSLKT**
RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**EDRLLGGYGYDV**WGQGTLVTVSS

**Figure 1b (Continued)**

**3102_ VH4** (SEQ ID NO: 25):
QVQLQESGPGLVKPGETLSLTCTVS**GGSISGNYWS**WIRQAPGKGLEWIG**DYHGSTYYNPSLKG**RVT
ISVDTSKNQFSLKLSSVTAEDTAVYYCAR**EQYHWGLAWTGFDN**WGQGTLVTVSS

**3127_ VH5** (SEQ ID NO: 26):
QVQLVQSGAEVKKPGESLKISCKGS**GYSFSTSWVG**WVRQMPGKGLEWMGI**IDPDISYTSYSPSFQG**
QVTISADKSISTAYLQWSSLKASDTAMYYCAR**YLMGLGYDV**WGQGTLVTVSS

**3128_ VH2** (SEQ ID NO: 27):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSSSGMSVS**WIRQPPGKALEWLA**RIYSDDSKSYSTSLKT**
RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**AAHWNGPLFDV**WGQGTLVTVSS

**3129_ VH3** (SEQ ID NO: 28):
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSNYSMN**WVRQAPGKGLEWVS**YIYGGGSYTYYADSVK**
**G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**QAGMYFDV**WGQGTLVTVSS

**3130_ VH4** (SEQ ID NO: 29):
QVQLQESGPGLVKPGETLSLTCTVS**GGSIGYYWN**WIRQAPGKGLEWIG**HISRFGSTNYNPSLKG**RV
TISVDTSKNQFSLKLSSVTAEDTAVYYCAR**EYTGNDWYRQQGQHADY**WGQGTLVTVSS

**3131_ VH2** (SEQ ID NO: 30):
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSNSGVGVG**WIRQPPGKALEWLA**DIYSDTTKRYSTSLKT**
RLTISKDTSKNQVVLTMTNMDPVDTATYYCAR**YGEAYFDY**WGQGTLVTVSS

**6183_VH3** (SEQ ID NO: 92)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSGINMESTRIYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6184_VH3** (SEQ ID NO: 93)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISHDGNVKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6185_VH3** (SEQ ID NO: 94)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMNGDYISYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6186_VH3** (SEQ ID NO: 95)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINLSGSAKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**Figure 1b (Continued)**

**6187_VH3** (SEQ ID NO: 96)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISSNGDITYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6188_VH3** (SEQ ID NO: 97)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISTNGWQTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6189_VH3** (SEQ ID NO: 98)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAINMIGNVTNYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6190_VH3** (SEQ ID NO: 99)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSYINPNGMMTNYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6192_VH3** (SEQ ID NO: 100)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSVISPGGEAKSYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6195_VH3** (SEQ ID NO: 101)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISGNGGHTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6197_VH3** (SEQ ID NO: 102)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMDGVYKYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6200_VH3** (SEQ ID NO: 103)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISNNGNVTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6201_VH3** (SEQ ID NO: 104)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYYMNWVRQAPGKGLEWVSAISMHGDTTYYADSVK
GRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDLPLVYTGFAYWGQGTLVTVSS

**6204_VH3** (SEQ ID NO: 105)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSHIRKKNTSYTTEYAAS
VKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

**Figure 1b (Continued)**

**6214_VH3** (SEQ ID NO: 106)
QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSNIQRVGSTYYADSVKG
RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREDGSYMTDYFAYWGQGTLVTVSS

**3077_VH1B** (SEQ ID NO: 114)
QVQLVQSGAEVKKPGASVKVSCKAS**GYTFTSYSIN**WVRQAPGQGLEWMGY**IDPNRGNTNYAQKFQ**
**G**RVTMTRDTSISTAYMELSSLRSEDTAVYYCAR**EYIYFIHGMLDF**WGQGTLVTVSS

**3079_VH3** (SEQ ID NO: 115)
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSNYGMH**WVRQAPGKGLEWVS**NIRSDGSWTYYADSV**
**KG**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**RYWSKSHASVTDY**WGQGTLVTVSS

**3080_ VH3** (SEQ ID NO: 116)
QVQLVESGGGLVQPGGSLRLSCAAS**GFTFSSYGMH**WVRQAPGKGLEWVS**NIYSDGSNTFYADSVK**
**G**RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR**NMYRWPFHYFFDY**WGQGTLVTVSS

**Figure 2a**

**Variable Light Chain DNA**

**3076_Vl lambda 2** (SEQ ID NO: 31):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGT
GTACGGGTACTAGCAGCGATATTGGTGCTTATGTGTCTTGGTACCAGCAGCATCCCGGGAAGGC
GCCGAAACTTATGATTTATGAGGTTTCTTCTCGTCCCTCAGGCGTGAGCAACCGTTTTAGCGGAT
CCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAGCGGATT
ATTATTGCTCTTCTTATGATCTTACTCCTCCTGGTAAGGTGTTTGGCGGCGGCACGAAGTTAACC
GTTCTTGGCCAG

**3078_Vl lambda 3** (SEQ ID NO: 32):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCGCTTCTGATGTTGGTTCTCTTGATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGC
CAG

**3081_ Vk kappa 3** (SEQ ID NO: 33):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG
AGCTGCAGAGCGAGCCAGACTGGTTCTACTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTC
AAGCACCGCGTCTATTAATTTATGATGCTTCTAAGCGTGCAACTGGGGTCCCGGCGCGTTTTAGC
GGCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGA
CTTATTATTGCCATCAGTATTATAACGTTCCTCATACCTTTGGCCAGGGTACGAAAGTTGAAATTA
AACGTACG

**3085_ Vl lambda 1** (SEQ ID NO: 34):
GATATCGTGCTGACCCAGCCGCCTTCAGTGAGTGGCGCACCAGGTCAGCGTGTGACCATCTCGT
GTAGCGGCAGCAGCAGCAACATTGGTAATAATTATGTGTCTTGGTACCAGCAGTTGCCCGGGAC
GGCGCCGAAACTTCTGATTTATGGTGATGATCAGCGTCCCTCAGGCGTGCCGGATCGTTTTAGC
GGATCCAAAAGCGGCACCAGCGCGAGCCTTGCGATTACGGGCCTGCAAAGCGAAGACGAAGCG
GATTATTATTGCCAGTCTTATGGTACTTTTTCTTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACC
GTTCTTGGCCAG

**3086_Vk kappa 1** (SEQ ID NO: 35):
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTA
CCTGCAGAGCGAGCCAGAATATTTCTCAGTGGCTGAATTGGTACCAGCAGAAACCAGGTAAAGC
ACCGAAACTATTAATTTATGGTGCTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCT
CTGGATCCGGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTAT
TATTGCCAGCAGTATTATGATCTTCCTAATACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGT
ACG

**3087_ Vl lambda 3** (SEQ ID NO: 36):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTCGTCATTATTATGTTTATTGGTACCAGCAGAAACCCGGGCAGGCGCCA
GTTCTTGTGATTTATGGTGATTCTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCAA
CAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATTA
TTGCCAGACTTATACTGGTGGTGCTTCTCTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTG
GCCAG

**Figure 2a (Continued)**

**3088_ Vl lambda 3** (SEQ ID NO: 37):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTTATAATGGTACTTATGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCCAG

**3089_ Vk kappa 3** (SEQ ID NO: 38):
GATATCGTGCTGACCCAGAGCCCGGCGACCCTGAGCCTGTCTCCGGGCGAACGTGCGACCCTG
AGCTGCAGAGCGAGCCAGTCTGTTTCTTCTTCTTATCTGGCTTGGTACCAGCAGAAACCAGGTCA
AGCACCGCGTCTATTAATTTATGGTGCTTCTTCTCGTGCAACTGGGGTCCCGGCGCGTTTTAGCG
GCTCTGGATCCGGCACGGATTTTACCCTGACCATTAGCAGCCTGGAACCTGAAGACTTTGCGGT
TTATTATTGCCAGCAGGGTTATAATTCTCCTTTTACCTTTGGCCAGGGTACGAAAGTTGAAATTAA
ACGTACG

**3101_ Vl lambda 3** (SEQ ID NO: 39):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATTCTCTTGGTTCTTATTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTGGTGATGATACTAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCGGTTCTCGTACTGGTTATAATAATTCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTT
CTTGGCCAG

**3102_ V'l lambda 3** (SEQ ID NO: 40):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGATGATTCTGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCGGTGCTTATGCTATGCATATGACTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGC
CAG

**3127_ Vl lambda 2** (SEQ ID NO: 41):
GATATCGCACTGACCCAGCCAGCTTCAGTGAGCGGCTCACCAGGTCAGAGCATTACCATCTCGT
GTACGGGTACTAGCAGCGATGTTGGTGCTATTAATTATGTGTCTTGGTACCAGCAGCATCCCGG
GAAGGCGCCGAAACTTATGATTTATGATGTTAATAAGCGTCCCTCAGGCGTGCCGGATCGTTTTA
GCGGATCCAAAAGCGGCAACACCGCGAGCCTGACCATTAGCGGCCTGCAAGCGGAAGACGAAG
CGGATTATTATTGCGGTTCTTATACTATGCAGGTTGGTTCTTATGTGTTTGGCGGCGGCACGAAG
TTAACCGTTCTTGGCCAG

**3128_ Vl lambda 3** (SEQ ID NO: 42):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGCTCATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTGTTGTGATTTATGATGATAATGATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGGCTTATACTGGTGATGGTGGTCGTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCT
TGGCCAG

**Figure 2a (Continued)**

**3129_ Vl lambda 3** (SEQ ID NO: 43):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTTCTAAGGTTGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTATGATAATAAGCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTTATACTTTTGAGTCTGGTTCTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTT
CTTGGCCAG

**3130_ Vl lambda 3** (SEQ ID NO: 44):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTCATTATTATGTTGATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGCTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCTCTTCTTATTCTCAGCAGTCTATGGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGC
CAG

**3131_ Vl lambda 3** (SEQ ID NO: 45):
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATCTTGGTAATTTTTATGTTCATTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATGAGGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCTCTTCTTGGGATATGTATCGTACTATTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTC
TTGGCCAG

**6278_Vl lambda 3** (SEQ ID NO: 107)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTGCTGATAATTTTCCTTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTCCTAGGT
CAG

**6279_ Vl lambda 3** (SEQ ID NO: 108)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTCATTATTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTCTTGTGATTTATTCTGATTCTAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCCAGTCTTATACTATGTCTGATGTTCTTGTTGTGTTTGGCGGCGGCACGAAGTTAACCGTC
CTAGGTCAG

**3077_Vk kappa 2** (SEQ ID NO: 117)
GATATCGTGATGACCCAGAGCCCACTGAGCCTGCCAGTGACTCCGGGCGAGCCTGCGAGCATT
AGCTGCAGAAGCAGCCAAAGCCTGCTTTTTATTGATGGCAATAATTATCTGAATTGGTACCTTCAA
AAACCAGGTCAAAGCCCGCAGCTATTAATTTATCTTGGTTCTAATCGTGCCAGTGGGGTCCCGGA
TCGTTTTAGCGGCTCTGGATCCGGCACCGATTTTACCCTGAAAATTAGCCGTGTGGAAGCTGAA
GACGTGGGCGTGTATTATTGCCAGCAGTATTCTTCTAAGTCTGCTACCTTTGGCCAGGGTACGAA
AGTTGAAATTAAACGTACG

**Figure 2a (Continued)**

**3079_Vk kappa 1** (SEQ ID NO: 118)
GATATCCAGATGACCCAGAGCCCGTCTAGCCTGAGCGCGAGCGTGGGTGATCGTGTGACCATTA
CCTGCAGAGCGAGCCAGGATATTTCTGCTTTTCTGAATTGGTACCAGCAGAAACCAGGTAAAGCA
CCGAAACTATTAATTTATAAGGTTTCTAATTTGCAAAGCGGGGTCCCGTCCCGTTTTAGCGGCTC
TGGATCCGGCACTGATTTTACCCTGACCATTAGCAGCCTGCAACCTGAAGACTTTGCGACTTATT
ATTGCCAGCAGGCTTATTCTGGTTCTATTACCTTTGGCCAGGGTACGAAAGTTGAAATTAAACGT
ACG

**3080_Vl lambda 3** (SEQ ID NO: 119)
GATATCGAACTGACCCAGCCGCCTTCAGTGAGCGTTGCACCAGGTCAGACCGCGCGTATCTCGT
GTAGCGGCGATAATATTGGTAATAAGTATGTTTCTTGGTACCAGCAGAAACCCGGGCAGGCGCC
AGTTGTTGTGATTTATGGTGATAATAATCGTCCCTCAGGCATCCCGGAACGCTTTAGCGGATCCA
ACAGCGGCAACACCGCGACCCTGACCATTAGCGGCACTCAGGCGGAAGACGAAGCGGATTATT
ATTGCTCTTCTTATGATTCTTCTTATTTTGTGTTTGGCGGCGGCACGAAGTTAACCGTTCTTGGCC
AG

**Figure 2b**

**Variable Light Chain Peptide**

(CDR Regions in **Bold** or underlined)

**3076_Vl lambda 2** (SEQ ID NO: 46):
DIALTQPASVSGSPGQSITISC**TGTSSDIGAYVS**WYQQHPGKAPKLMIY**EVSSRPS**GVSNRFSGSKSG
NTASLTISGLQAEDEADYYC**SSYDLTPPGK**VFGGGTKLTVLGQ

**3078_Vl lambda 3** (SEQ ID NO: 47):
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**GDNNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**ASDVGSLD**VFGGGTKLTVLGQ

**3081_ Vk kappa 3** (SEQ ID NO: 48):
DIVLTQSPATLSLSPGERATLSC**RASQTGSTSYLA**WYQQKPGQAPRLLIY**DASKRAT**GVPARFSGSG
SGTDFTLTISSLEPEDFATYYC**HQYYNVPH**TFGQGTKVEIKRT

**3085_ Vl lambda 1** (SEQ ID NO: 49):
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGNNYVS**WYQQLPGTAPKLLIY**GDDQRPS**GVPDRFSGSK
SGTSASLAITGLQSEDEADYYC**QSYGTFSSF**VFGGGTKLTVLGQ

**3086_Vk kappa 1** (SEQ ID NO: 50):
DIQMTQSPSSLSASVGDRVTITC**RASQNISQWLN**WYQQKPGKAPKLLIY**GASNLQS**GVPSRFSGSG
SGTDFTLTISSLQPEDFATYYC**QQYYDLPN**TFGQGTKVEIKRT

**3087_ Vl lambda 3** (SEQ ID NO: 51):
DIELTQPPSVSVAPGQTARISC**SGDNLRHYYVY**WYQQKPGQAPVLVIY**GDSKRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QTYTGGASL**VFGGGTKLTVLGQ

**3088_ Vl lambda 3** (SEQ ID NO: 52):
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**SDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QSYNGTY**VFGGGTKLTVLGQ

**3089_ Vk kappa 3** (SEQ ID NO: 53):
DIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRLLIY**GASSRAT**GVPARFSGSG
SGTDFTLTISSLEPEDFAVYYC**QQGYNSPF**TFGQGTKVEIKRT

**3101_ Vl lambda 3** (SEQ ID NO: 54):
DIELTQPPSVSVAPGQTARISC**SGDSLGSYYVH**WYQQKPGQAPVLVIG**DDTKRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**GSRTGYNNSF**VFGGGTKLTVLGQ

**3102_ Vl lambda 3** (SEQ ID NO: 55):
DIELTQPPSVSVAPGQTARISC**SGDNLGHYYVS**WYQQKPGQAPVLVIY**DDSDRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**GAYAMHMT**VFGGGTKLTVLGQ

**3127_ Vl lambda 2** (SEQ ID NO: 56):
DIALTQPASVSGSPGQSITISC**TGTSSDVGAINYVS**WYQQHPGKAPKLMIY**DVNKRPS**GVPDRFSGS
KSGNTASLTISGLQAEDEADYYC**GSYTMQVGSY**VFGGGTKLTVLGQ

**Figure 2b (Continued)**

**3128_ Vl lambda 3** (SEQ ID NO: 57):
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYAH**WYQQKPGQAPVVVIY**DDNDRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCQ**AYTGDGGR**VFGGGTKLTVLGQ

**3129_ Vl lambda 3** (SEQ ID NO: 58):
DIELTQPPSVSVAPGQTARISC**SGDNLGSKVVS**WYQQKPGQAPVLVIY**YDNKRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCQ**SYTFESGSV**VFGGGTKLTVLGQ

**3130_ Vl lambda 3** (SEQ ID NO: 59):
DIELTQPPSVSVAPGQTARISC**SGDNLGHYYVD**WYQQKPGQAPVLVIY**ADNNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCS**SYSQQSM**VFGGGTKLTVLGQ

**3131_ Vl lambda 3** (SEQ ID NO: 60):
DIELTQPPSVSVAPGQTARISC**SGDNLGNFYVH**WYQQKPGQAPVLVIY**EDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYCS**SWDMYRTIF**VFGGGTKLTVLGQ

**6278_ Vl lambda 3** (SEQ ID NO: 109)
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**SDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QSADNFPF**VFGGGTKLTVLGQ

**6279_ Vl lambda 3** (SEQ ID NO: 110)
DIELTQPPSVSVAPGQTARISC**SGDNIGHYYVS**WYQQKPGQAPVLVIY**SDSNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**QSYTMSDVLV**VFGGGTKLTVLGQ

**3077_Vk kappa 2** (SEQ ID NO: 120)
DIVMTQSPLSLPVTPGEPASISC**RSSQSLLFIDGNNYLN**WYLQKPGQSPQLLIY**LGSNRAS**GVPDRFS
GSGSGTDFTLKISRVEAEDVGVYYC**QQYSSKSA**TFGQGTKVEIKRT

**3079_Vk kappa 1** (SEQ ID NO: 121)
DIQMTQSPSSLSASVGDRVTITC**RASQDISAFLN**WYQQKPGKAPKLLIY**KVSNLQS**GVPSRFSGSGS
GTDFTLTISSLQPEDFATYYC**QQAYSGSI**TFGQGTKVEIKRT

**3080_Vl lambda3** (SEQ ID NO: 122)
DIELTQPPSVSVAPGQTARISC**SGDNIGNKYVS**WYQQKPGQAPVVVIY**GDNNRPS**GIPERFSGSNSG
NTATLTISGTQAEDEADYYC**SSYDSSYF**VFGGGTKLTVLGQ

**Figure 3**

**Variable Heavy Chain Consensus Sequences**

(CDR Regions in **Bold**)

**VH1A Consensus (SEQ ID NO: 61):**
QVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYAIS**WVRQAPGQGLEWMG**GIIPIFGTANYAQKFQG**RV
TITADESTSTAYMELSSLRSEDTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

**VH2 Consensus (SEQ ID NO: 62)**
QVQLKESGPALVKPTQTLTLTCTFS**GFSLSTSGVGVG**WIRQPPGKALEWLA**LIDWDDDKYYSTSLKT**R
LTISKDTSKNQVVLTMTNMDPVDTATYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

**VH3 Consensus** (SEQ ID NO: 63):

(1) QVQLVESGGG LVQPGGSLRL SCAAS**GFTFS SYAMS**WVRQA PGKGLEWVS**A**
(51) **ISGSGGSTYY ADSVKG**RFTI SRDNSKNTLY LQMNSLRAED TAVYYCAR**WG**
(101) **GDGFYAMDY**W GQGTLVTVS S

**VH4 Consensus** (SEQ ID NO: 64):
QVQLQESGPGLVKPSETLSLTCTVS**GGSISSYYWS**WIRQPPGKGLEWIG**YIYYSGSTNYNPSLKS**RVT
ISVDTSKNQFSLKLSSVTAADTAVYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

**VH5 Consensus** (SEQ ID NO: 65):
QVQLVQSGAEVKKPGESLKISCKGS**GYSFTSYWIG**WVRQMPGKGLEWMG**IIYPGDSDTRYSPSFQGQ**V
TISADKSISTAYLQWSSLKASDTAMYYCAR**WGGDGFYAMDY**WGQGTLVTVSS

**Figure 4**

**Variable Light Chain Consensus Sequences**

(CDR Regions in **Bold**)

**Vl_λ1 Consensus (SEQ ID NO: 66):**
DIVLTQPPSVSGAPGQRVTISC**SGSSSNIGSNYVS**WYQQLPGTAPKLLIY**DNNQRPS**GVPDRFSGSKS
GTSASLAITGLQSEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

**Vl_λ2 Consensus (SEQ ID NO: 67):**
DIALTQPASVSGSPGQSITISC**TGTSSDVGGYNYVS**WYQQHPGKAPKLMIY**DVSNRPS**GVSNRFSGSK
SGNTASLTISGLQAEDEADYYC**QQHYTTPP**VFGGGTKLTVLGQ

**Vl_λ3 Consensus** (SEQ ID NO: 68):

(1) DIELTQPPSV SVAPGQTARI SC**SGDALGDK YAS**WYQQKPG QAPVLVIY**DD**
(51) **SDRPS**GIPER FSGSNSGNTA TLTISGTQAE DEADYYC**QQH YTTPP**VFGGG
(101) TKLTVLG

**Vl_k1 Consensus** (SEQ ID NO: 69):

(1) DIQMTQSPSS LSASVGDRVT ITC**RASQGIS SYLA**WYQQKP GKAPKLLIY**A**
(51) **ASSLQS**GVPS RFSGSGSGTD FTLTISSLQP EDFATYYC**QQ HYTTP**PTFGQ
(101) GTKVEIKR

**Vl_k3 Consensus** (SEQ ID NO: 70):
DIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRLLIY**GASSRAT**GVPARFSGSGS
GTDFTLTISSLEPEDFAVYYC**QQHYTTPP**TFGQGTKVEIKRT

**Figure 5**

**Peptide Sequence of CD38**

(SEQ ID NO: 71):

1 mancefspvs gdkpccrlsr raqlclgvsi lvlilvvvla vvvprwrqqw sgpgttkrfp

61 etvlarcvky teihpemrhv dcqsvwdafk gafiskhpcn iteedyqplm klgtqtvpcn

121 killwsrikd lahqftqvqr dmftledtll gyladdltwc gefntskiny qscpdwrkdc

181 snnpvsvfwk tvsrrfaeaa cdvvhvmlng srskifdkns tfgsvevhnl qpekvqtlea

241 wvihggreds rdlcqdptik elesiiskrn iqfsckniyr pdkflqcvkn pedssctsei

**Figure 6**

**Nucleotide Sequence of Chimeric OKT10**

Heavy Chain (SEQ ID NO: 72):

caggtggaat tggtggaatc tggaggatcc ctgaaactct cctgtgcagc ctcaggattc

gattttagta gatcctggat gaattgggtc cggcaggctc caggaaaagg gctagaatgg

attggagaaa ttaatccaga tagcagtacg ataaactata cgacatctct aaaggataaa

ttcatcatct ccagagacaa cgccaaaaat acgctgtacc tgcaaatgac caaagtgaga

tctgaggaca cagcccttta ttactgtgca agatatggta actggtttcc ttattggggc

caagggactc tggtcactgt cagctcagcc tccaccaagg gtccatcggt cttccccctg

gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac

tacttccccg aaccggtgac ggtgtcgtgg aactcaggcg ccctgaccag cggcgtgcac

accttcccgg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg

ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacaa gcccagcaac

accaaggtgg acaagaaagt tgagcccaaa tcttgtgaca aaactcacac atgcccaccg

tgcccagcac ctgaactcct gggggggaccg tcagtcttcc tcttcccccc aaaacccaag

gacaccctca tgatctcccg gacccctgag gtcacatgcg tggtggtgga cgtgagccac

gaagaccctg aggtcaagtt caactggtac gtggacggcg tggaggtgca taatgccaag

acaaagccgc gggaggagca gtacaacagc acgtaccggg tggtcagcgt cctcaccgtc

ctgcaccagg actggctgaa tggcaaggag tacaagtgca aggtctccaa caaagccctc

ccagccccca tcgagaaaac catctccaaa gccaaagggc agccccgaga accacaggtg

tacaccctgc ccccatcccg ggatgagctg accaagaacc aggtcagcct gacctgcctg

gtcaaaggct tctatcccag cgacatcgcc gtggagtggg agagcaatgg gcagccggag

aacaactaca agaccacgcc tcccgtgctg gactccgacg gctccttctt cctctacagc

aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg

catgaggctc tgcacaacca ctacacgcag aagagcctct ccctgtctcc gggtaaa

**Figure 6 (Continued)**

Light Chain (SEQ ID NO: 73):

gatatcctga tgacccagtc tcaaaaaatc atgcccacat cagtgggaga cagggtcagc

gtcacctgca aggccagtca aaatgtggat actaatgtag cctggtatca acagaaacca

ggacagtctc ctaaagcact gatttactcg gcatcctacc gatacagtgg agtccctgat

cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcaccaa tgtgcagtct

gaggacttgg cagagtattt ctgtcagcaa tatgacagct atcctctcac gttcggtgct

gggaccaagc tggacctgaa acgtacggtg gctgcaccat ctgtcttcat cttcccgcca

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt

**Figure 7: DNA sequence of pMOPRH®_h_IgG1_1**

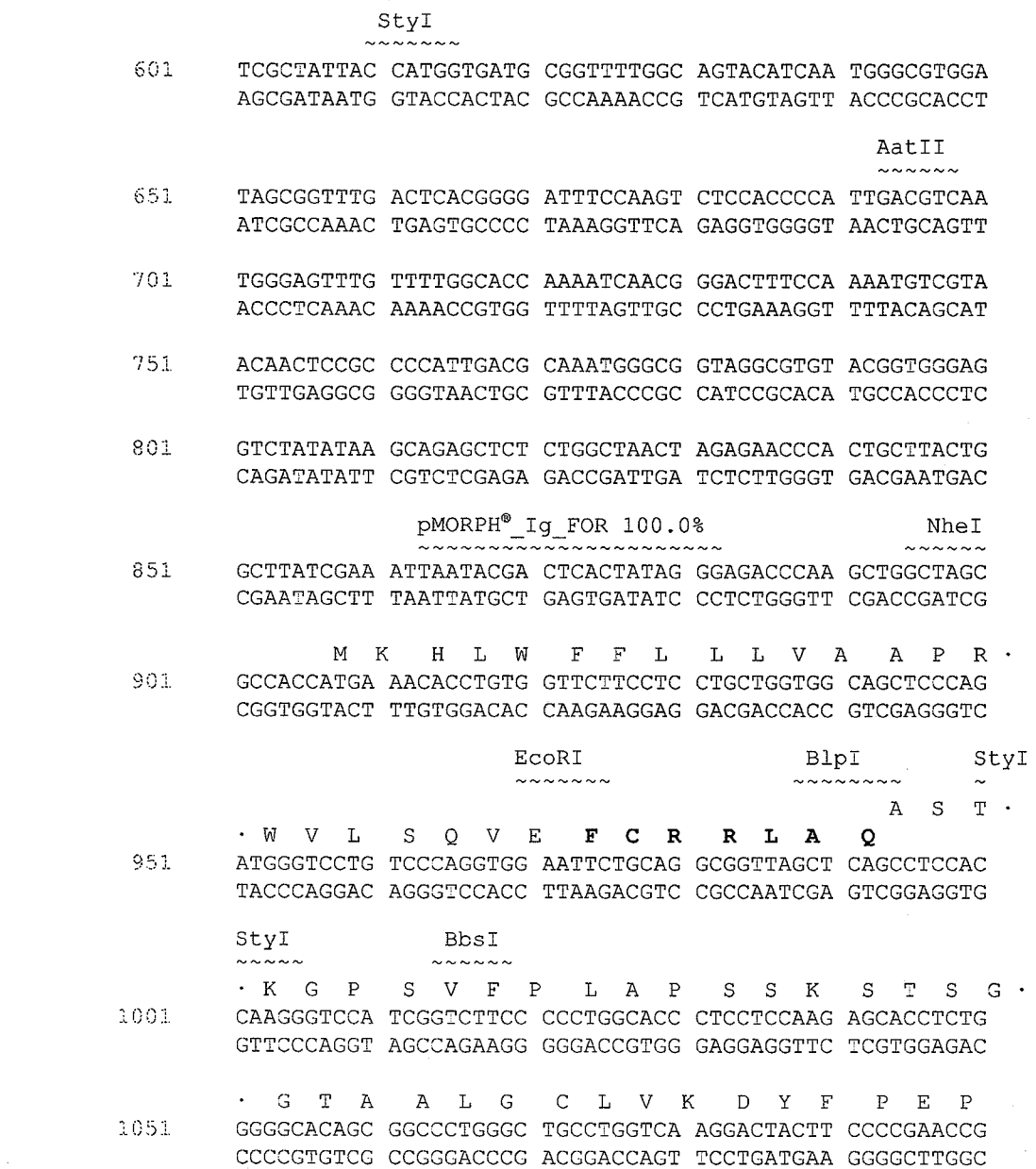


**Figure 7 (Continued)**

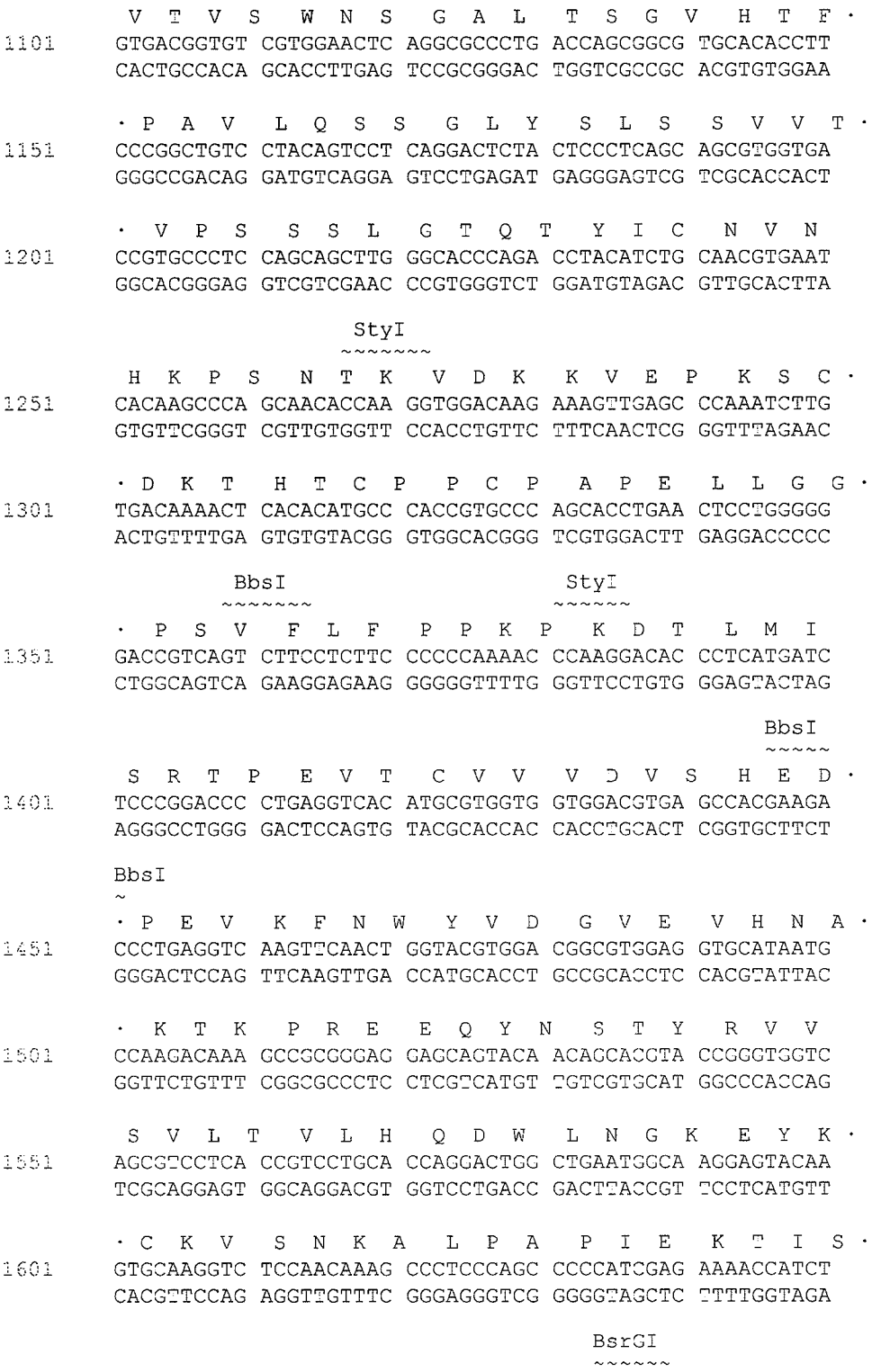


**Figure 7 (Continued)**

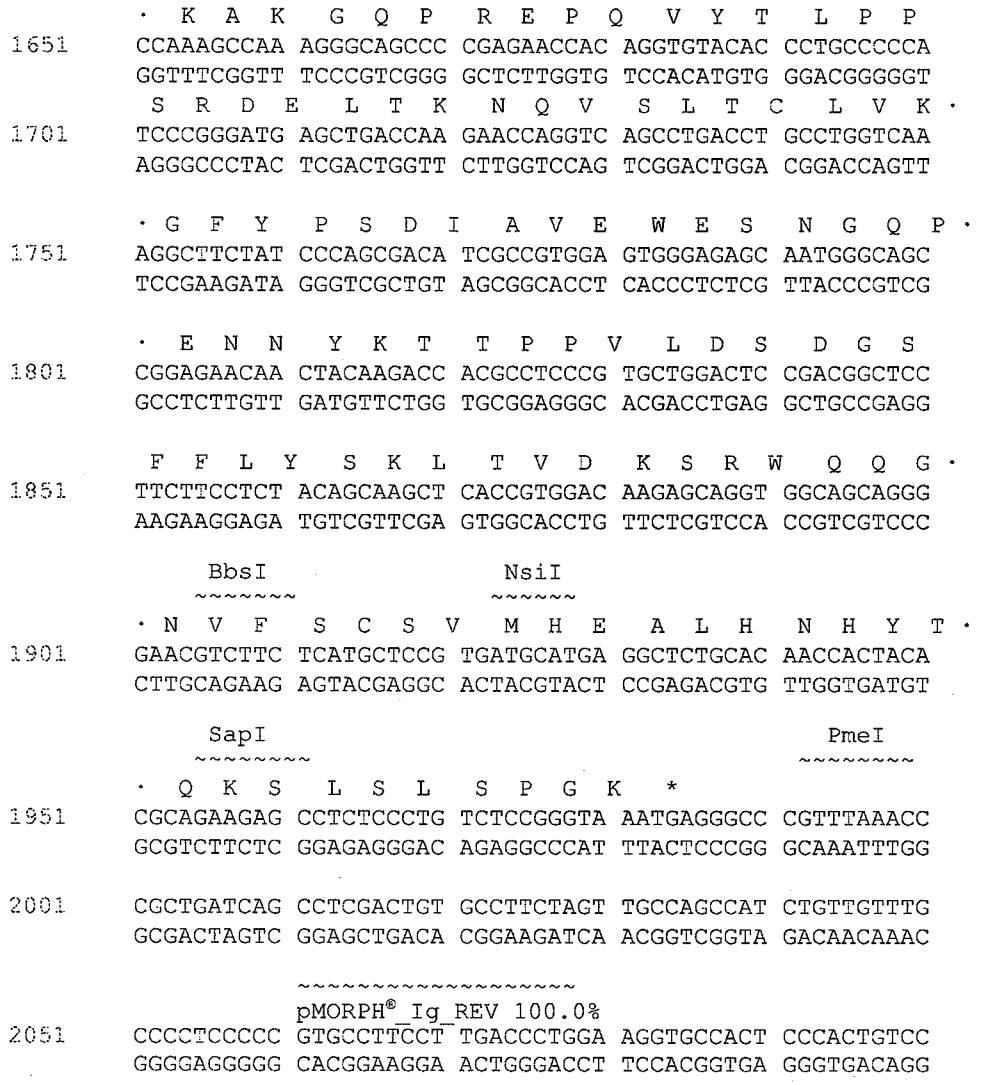


**Figure 8: DNA Sequence of Ig kappa light chain expression vector pMORPH®_h_Igκ_1**

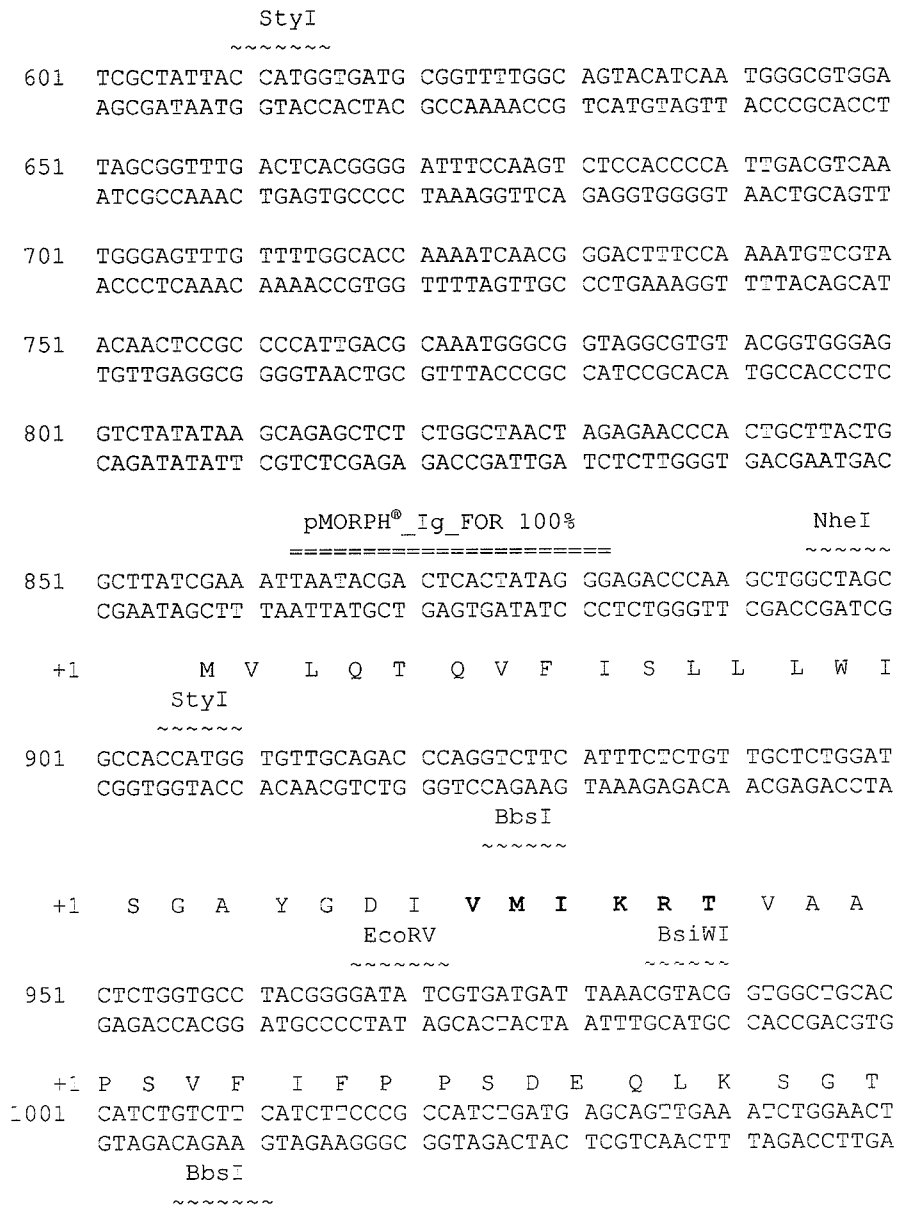


**Figure 8 (Continued)**

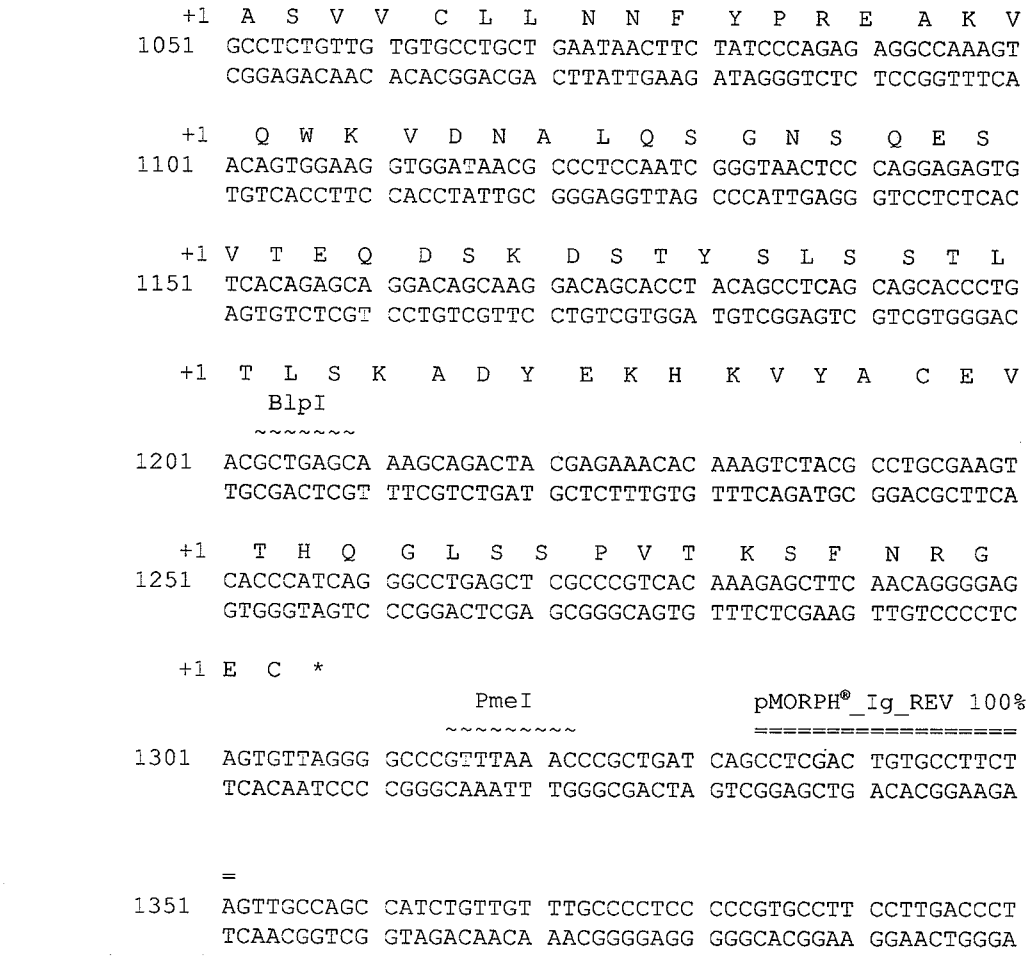


**Figure 9: DNA Sequence of HuCAL® Ig lambda light chain vector pMORPH®_h_Igλ_1**

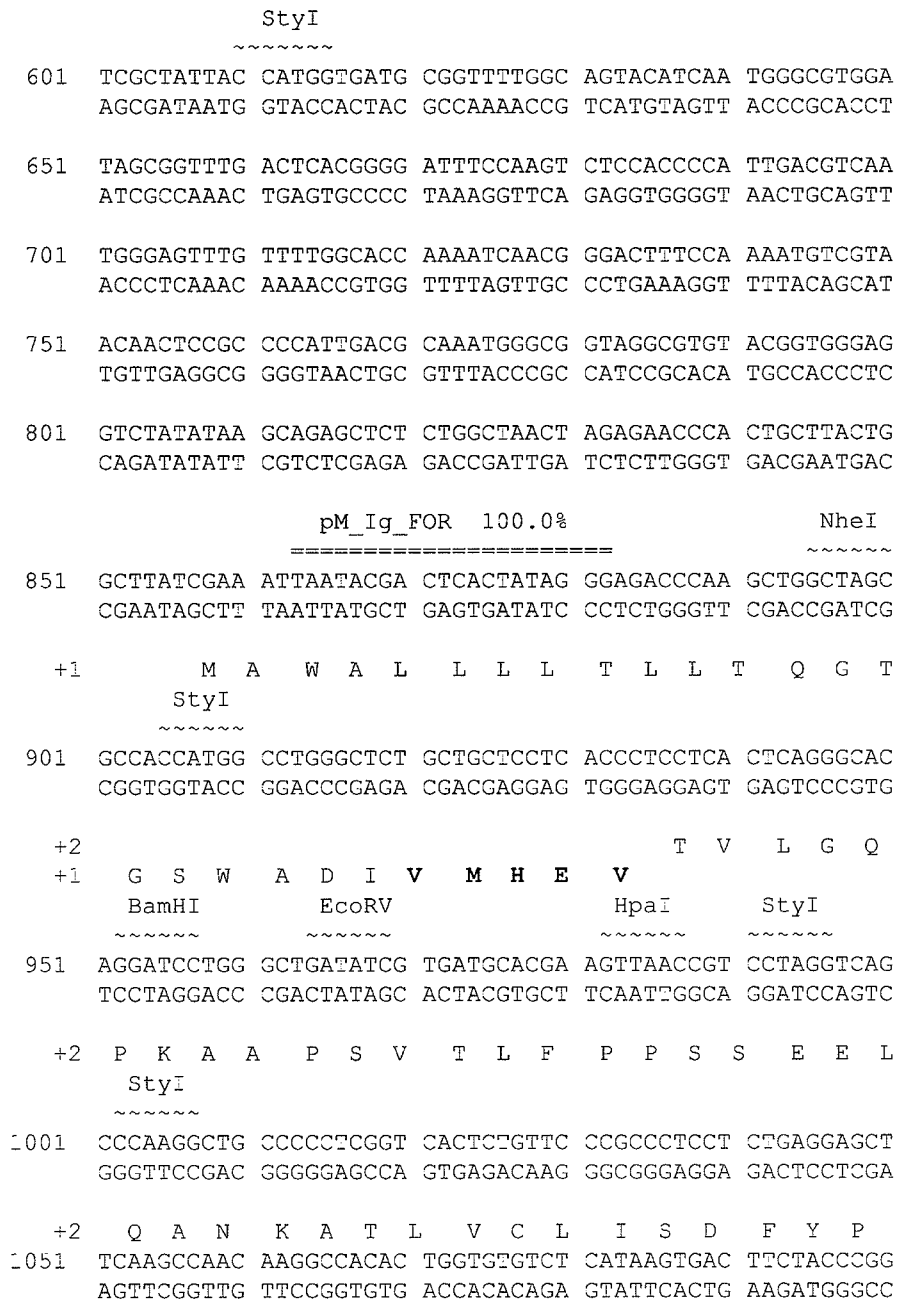


**Figure 9 (Continued)**

```
   +2 G  A  V  T   V  A  W   K  G  D  S   S  P  V   K  A  G
1101  GAGCCGTGAC AGTGGCCTGG AAGGGAGATA GCAGCCCCGT CAAGGCGGGA
      CTCGGCACTG TCACCGGACC TTCCCTCTAT CGTCGGGGCA GTTCCGCCCT

   +2  V  E  T  T   T  P  S   K  Q  S   N  N  K  Y   A  A  S
1151  GTGGAGACCA CCACACCCTC CAAACAAAGC AACAACAAGT ACGCGGCCAG
      CACCTCTGGT GGTGTGGGAG GTTTGTTTCG TTGTTGTTCA TGCGCCGGTC

   +2   S  Y  L   S  L  T  P   E  Q  W   K  S  H   R  S  Y
1201  CAGCTATCTG AGCCTGACGC CTGAGCAGTG GAAGTCCCAC AGAAGCTACA
      GTCGATAGAC TCGGACTGCG GACTCGTCAC CTTCAGGGTG TCTTCGATGT

   +2 S  C  Q  V   T  H  E   G  S  T  V   E  K  T   V  A  P
                                          BbsI
                                          ~~~~~~
1251  GCTGCCAGGT CACGCATGAA GGGAGCACCG TGGAGAAGAC AGTGGCCCCT
      CGACGGTCCA GTGCGTACTT CCCTCGTGGC ACCTCTTCTG TCACCGGGGA

   +2  T  E  C  S   *
                        PmeI
                       ~~~~~~~~
1301  ACAGAATGTT CATAGGGGCC CGTTTAAACC CGCTGATCAG CCTCGACTGT
      TGTCTTACAA GTATCCCCGG GCAAATTTGG GCGACTAGTC GGAGCTGACA
                                              pM_Ig_REV 100%
                                                 ==========

1351  GCCTTCTAGT TGCCAGCCAT CTGTTGTTTG CCCCTCCCCC GTGCCTTCCT
      CGGAAGATCA ACGGTCGGTA GACAACAAAC GGGGAGGGGG CACGGAAGGA
      pM_Ig_REV  100.0%
 =========
```

**Figure 10**

| Designation: | Format | Affinity Maturation | Heavy chain from: | Light chain from: |
|---|---|---|---|---|
| MOR06183 | Fab/IgG1 | new H-CDR2 | MOR06183 | MOR03087 (parental) |
| MOR06184 | Fab/IgG1 | new H-CDR2 | MOR06184 | MOR03087 (parental) |
| MOR06185 | Fab/IgG1 | new H-CDR2 | MOR06185 | MOR03087 (parental) |
| MOR06186 | Fab/IgG1 | new H-CDR2 | MOR06186 | MOR03087 (parental) |
| MOR06187 | Fab/IgG1 | new H-CDR2 | MOR06187 | MOR03087 (parental) |
| MOR06188 | Fab/IgG1 | new H-CDR2 | MOR06188 | MOR03087 (parental) |
| MOR06189 | Fab/IgG1 | new H-CDR2 | MOR06189 | MOR03087 (parental) |
| MOR06190 | Fab/IgG1 | new H-CDR2 | MOR06190 | MOR03087 (parental) |
| MOR06192 | Fab/IgG1 | new H-CDR2 | MOR06192 | MOR03087 (parental) |
| MOR06195 | Fab/IgG1 | new H-CDR2 | MOR06195 | MOR03087 (parental) |
| MOR06197 | Fab/IgG1 | new H-CDR2 | MOR06197 | MOR03087 (parental) |
| MOR06200 | Fab/IgG1 | new H-CDR2 | MOR06200 | MOR03087 (parental) |
| MOR06201 | Fab/IgG1 | new H-CDR2 | MOR06201 | MOR03087 (parental) |
| MOR06204 | Fab/IgG1 | new H-CDR2 | MOR06204 | MOR03088 (parental) |
| MOR06214 | Fab/IgG1 | new H-CDR2 | MOR06214 | MOR03088 (parental) |
| MOR06278 | Fab | new L-CDR3 | MOR03088 (parental) | MOR06278 |
| MOR06279 | Fab | new L-CDR3 | MOR03088 (parental) | MOR06279 |
| MOR06347 | IgG1 | new L-CDR3 | MOR03088 (parental) | MOR06278 |
| MOR06348 | IgG1 | new L-CDR3 & H-CDR2 | MOR06214 | MOR06278 |

**FIGURE 11: CD38-expression analysis of Lymphocytes and Erythrocytes**

**A: MOR 3087**

**B: MOR 3088**

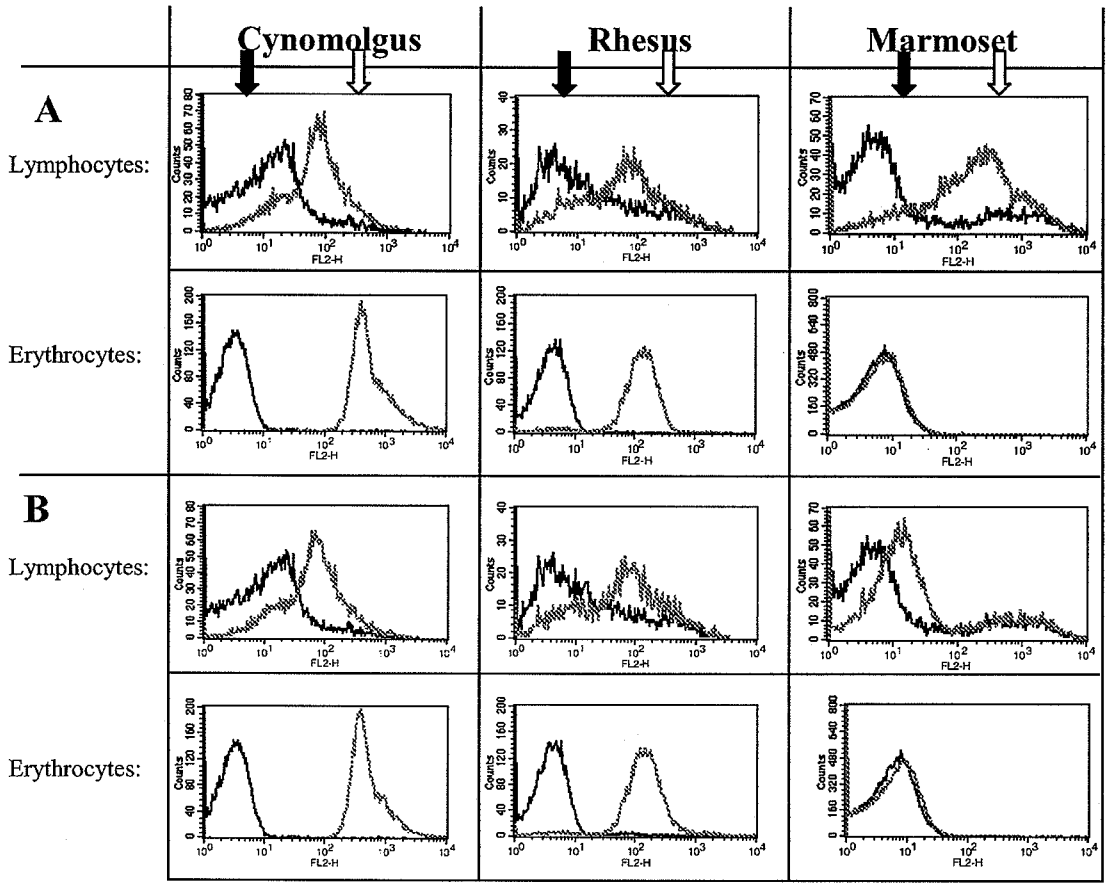


**Figure 12: CD38 expression analysis of Lymphocytes and Erythrocytes**

**MOR 03087:**

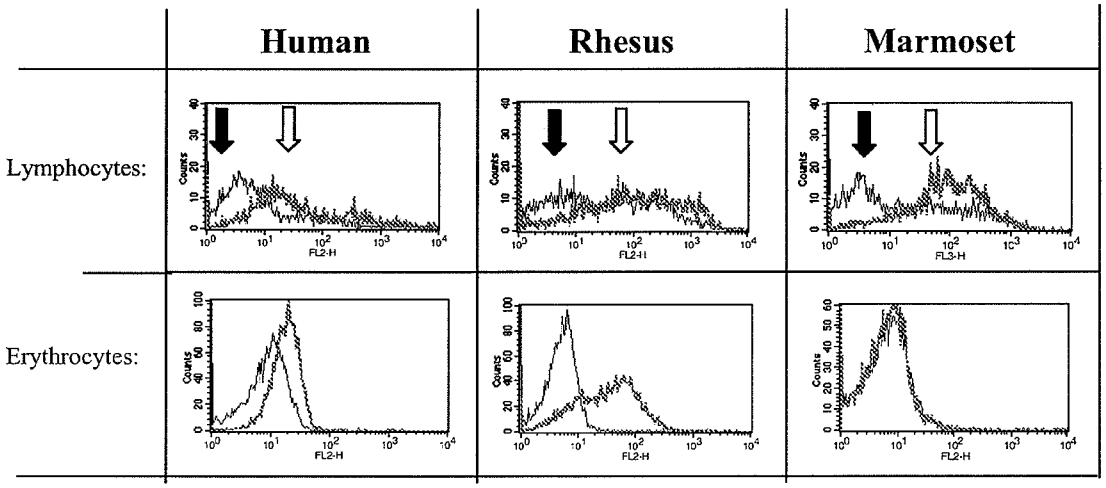
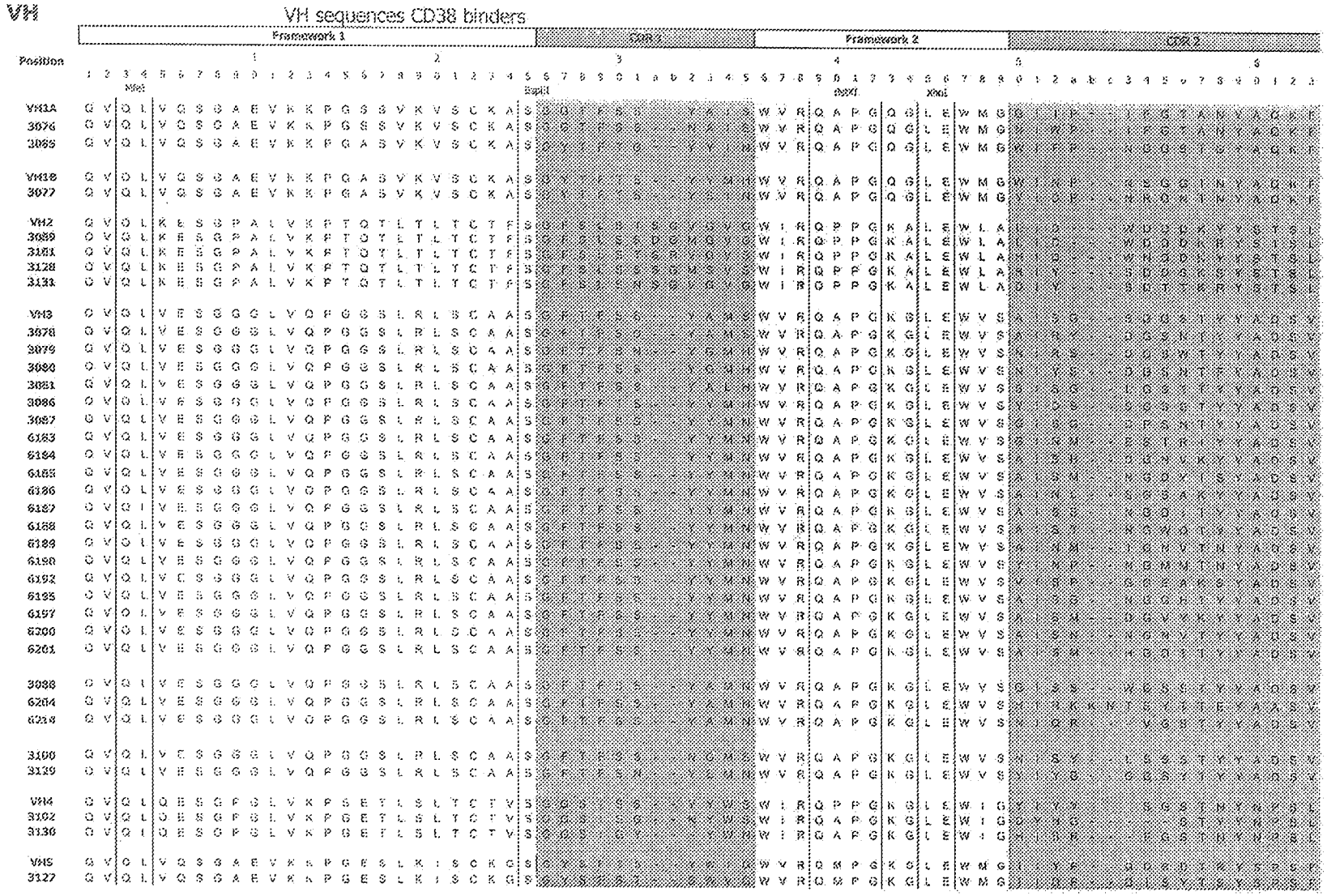


**Figure 13: Overview Cross-Reactivity Anti-CD38 Antibodies**

| | Human | | Rhesus | | Cynomolgus | | Marmoset | |
|---|---|---|---|---|---|---|---|---|
| Species/Tissue: / Anti-CD38 MAbs: | PBMCs | Erythr. | PBMCs | Erythr. | PBMCs | Erythr. | PBMCs | Erythr. |
| 3076 | + | n.d. | - | - | - | - | - | - |
| 3077 | + | - | - | - | - | - | - | - |
| 3078 | + | n.d. | - | - | - | - | - | - |
| 3079 | + | + | - | - | - | - | - | - |
| 3080 | + | +/- | + | - | + | - | - | - |
| 3081 | + | n.d. | - | - | - | - | - | - |
| 3085 | + | n.d. | - | - | - | - | - | - |
| 3086 | + | n.d. | - | - | - | - | - | - |
| 3087 | + | +/- | + | + | + | + | + | - |
| 3088 | + | - | + | + | + | + | + | - |
| 3089 | + | n.d. | - | - | - | - | - | - |
| 3101 | + | n.d. | - | - | - | - | - | - |
| 3102 | + | n.d. | - | - | - | - | - | - |
| 3127 | + | n.d. | - | - | - | - | - | - |
| 3128 | + | n.d. | - | - | - | - | - | - |
| 3129 | + | n.d. | - | - | - | - | - | - |
| 3130 | + | n.d. | - | - | - | - | - | - |
| 3131 | + | n.d. | - | - | - | - | - | - |

+ : positive staining
+/-: weak positive staining
- : negative staining
n.d.: not determined

Figure 14a


VH
VH sequences CD38 binders
Framework 1
CDR1
Framework 2
CDR2
Position
NheI
BspEI
BstXI
XhoI
VH1A
3076
3088
VH1B
3077
VH2
3089
3181
3128
3131
VH3
3078
3079
3080
3081
3086
3087
6183
6184
6185
6186
6187
6188
6189
6190
6192
6195
6197
6200
6201
3088
6204
6214
3100
3139
VH4
3102
3130
VH5
3127

## Figure 14a (Continued)

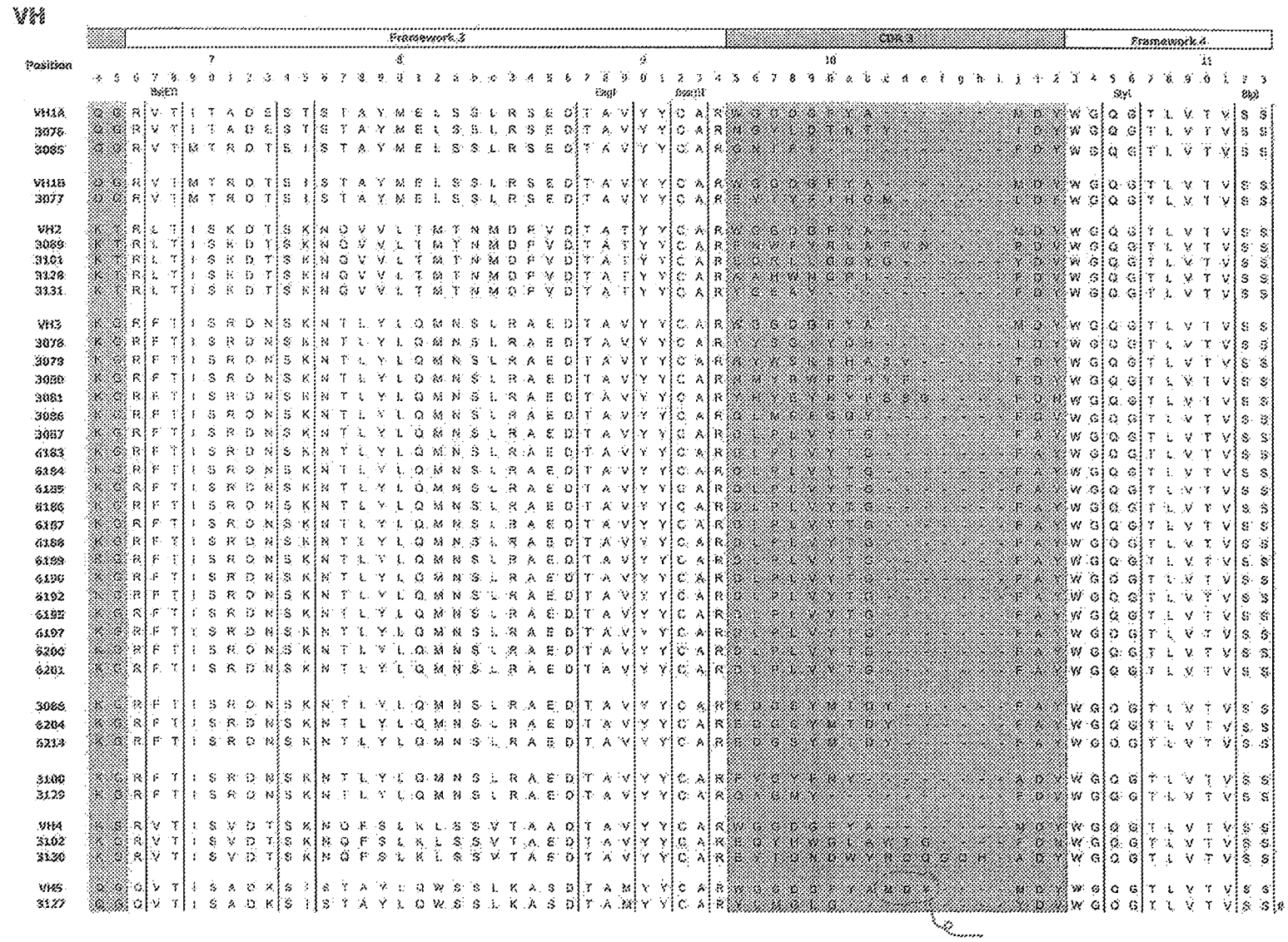


Figure 14b

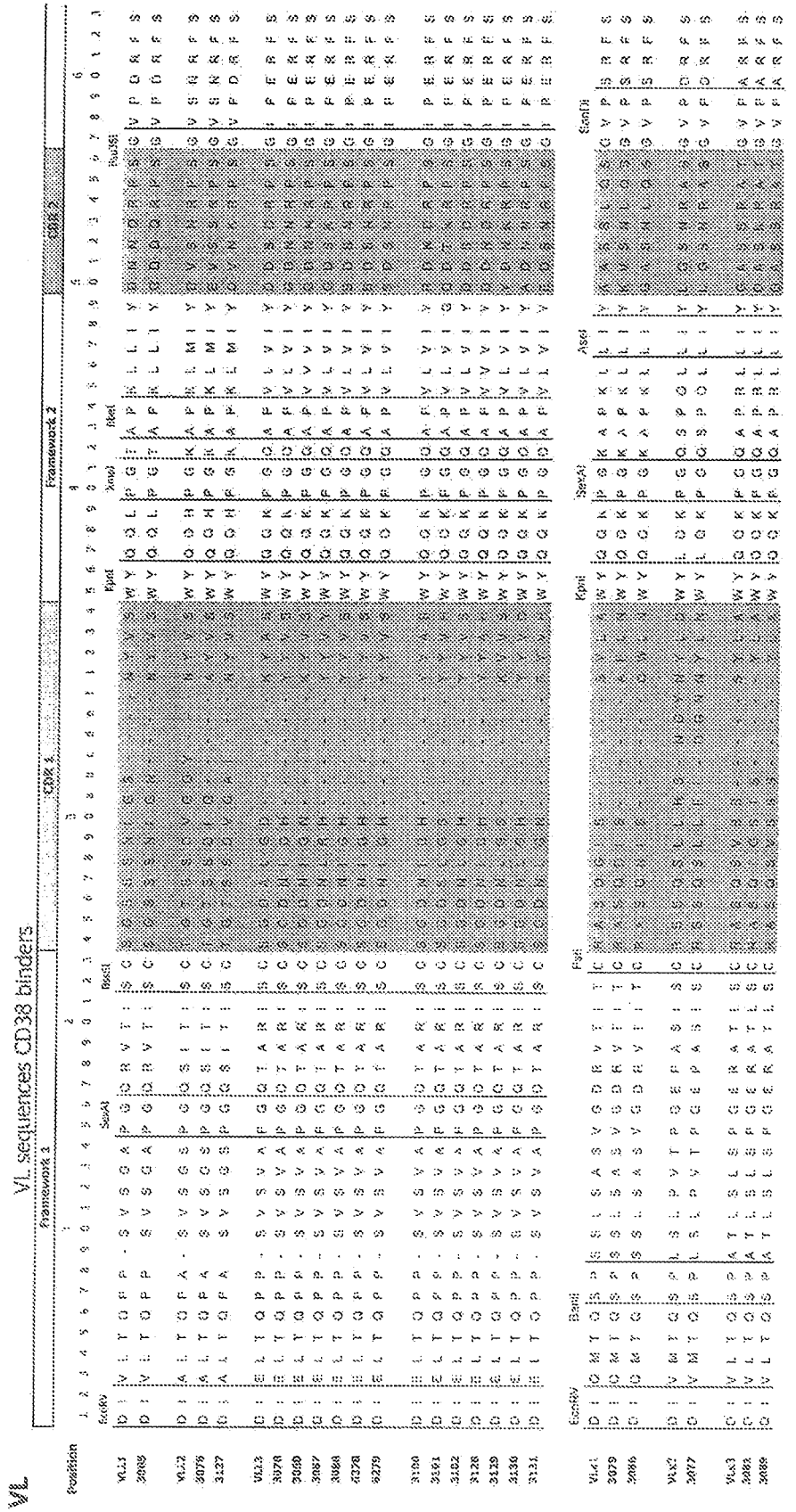

VL
VL sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Position
VLk1
3068
VLk2
3076
3127
VLk3
3078
3069
3087
3088
4078
9279
3100
3101
3102
3126
3129
3130
3131
VLk1
3079
3066
VLk2
3077
VLk3
3081
3089

Figure 14b (Continued)

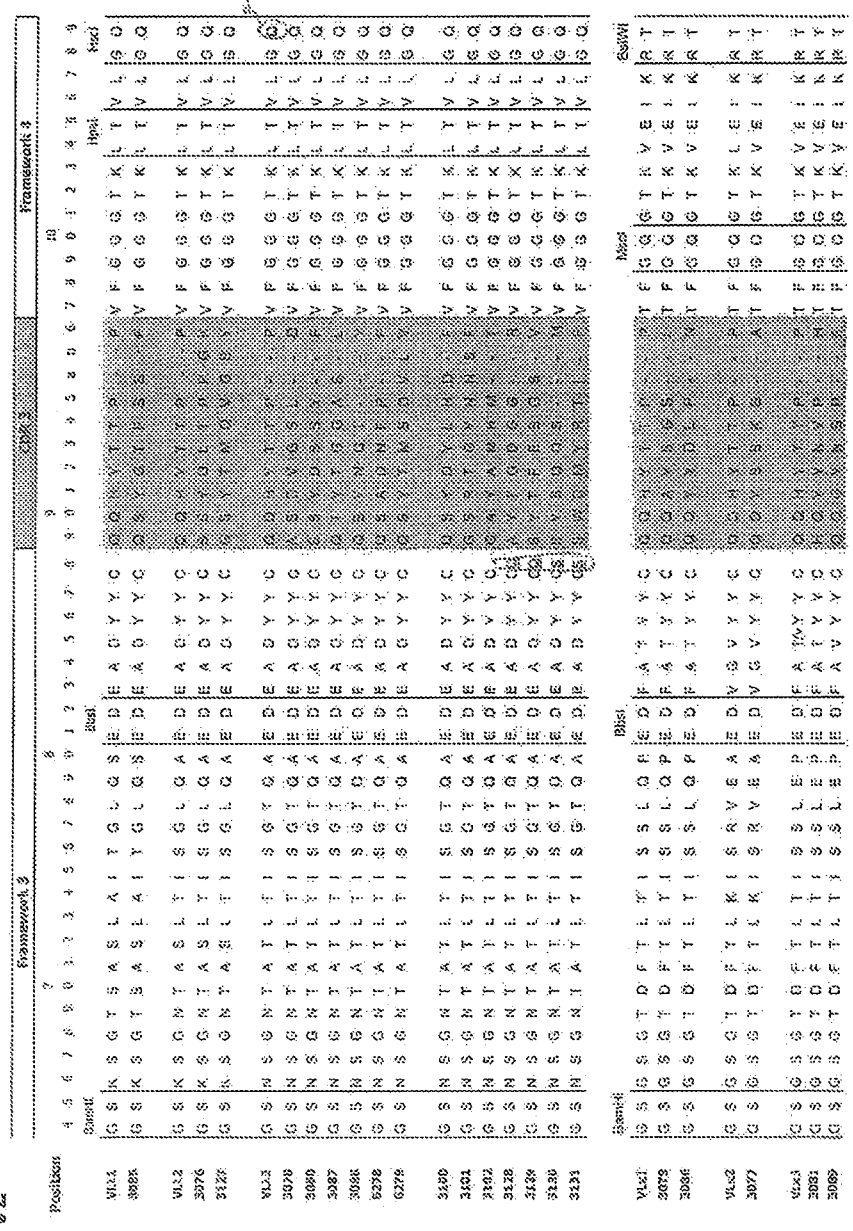


Figure 14a

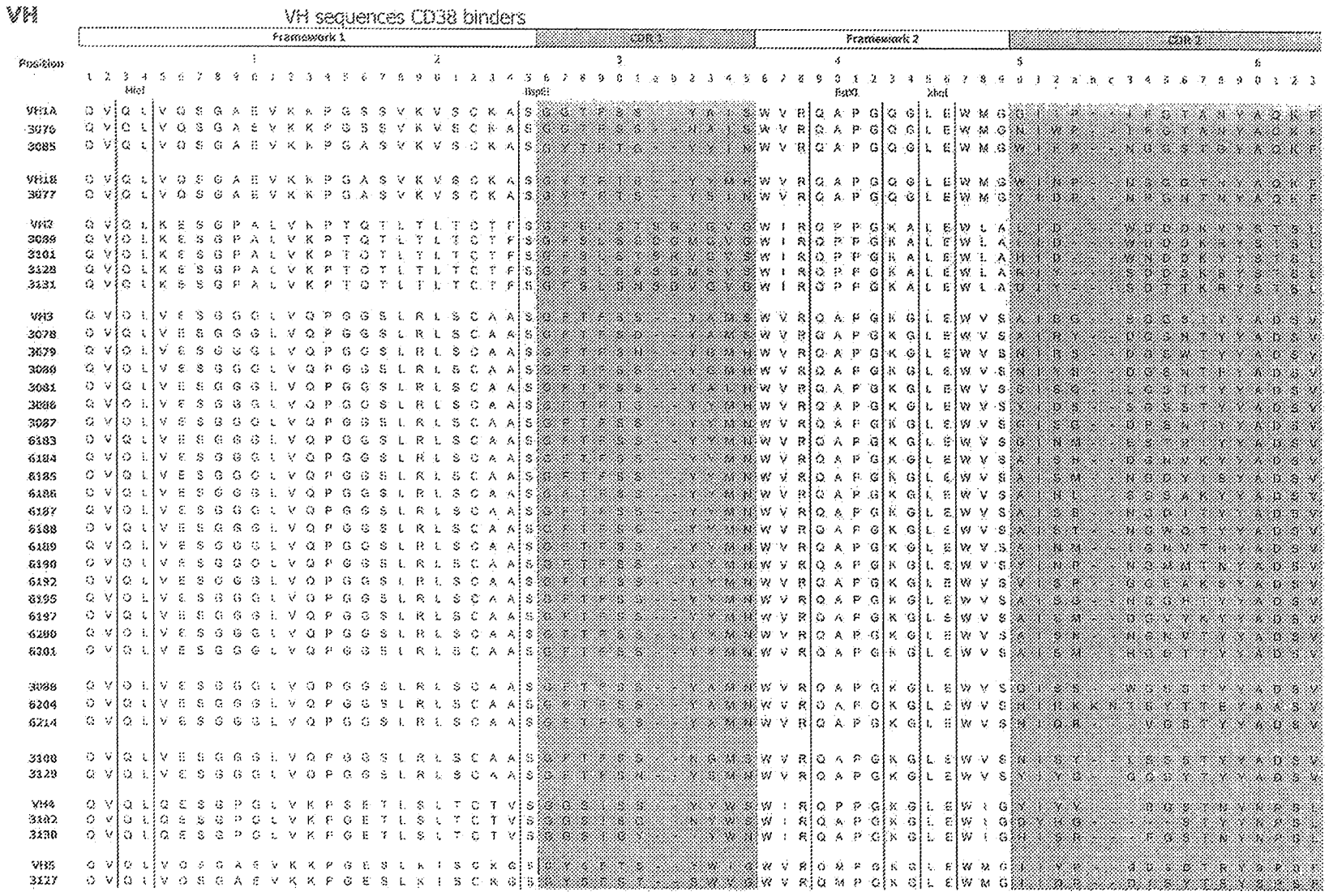
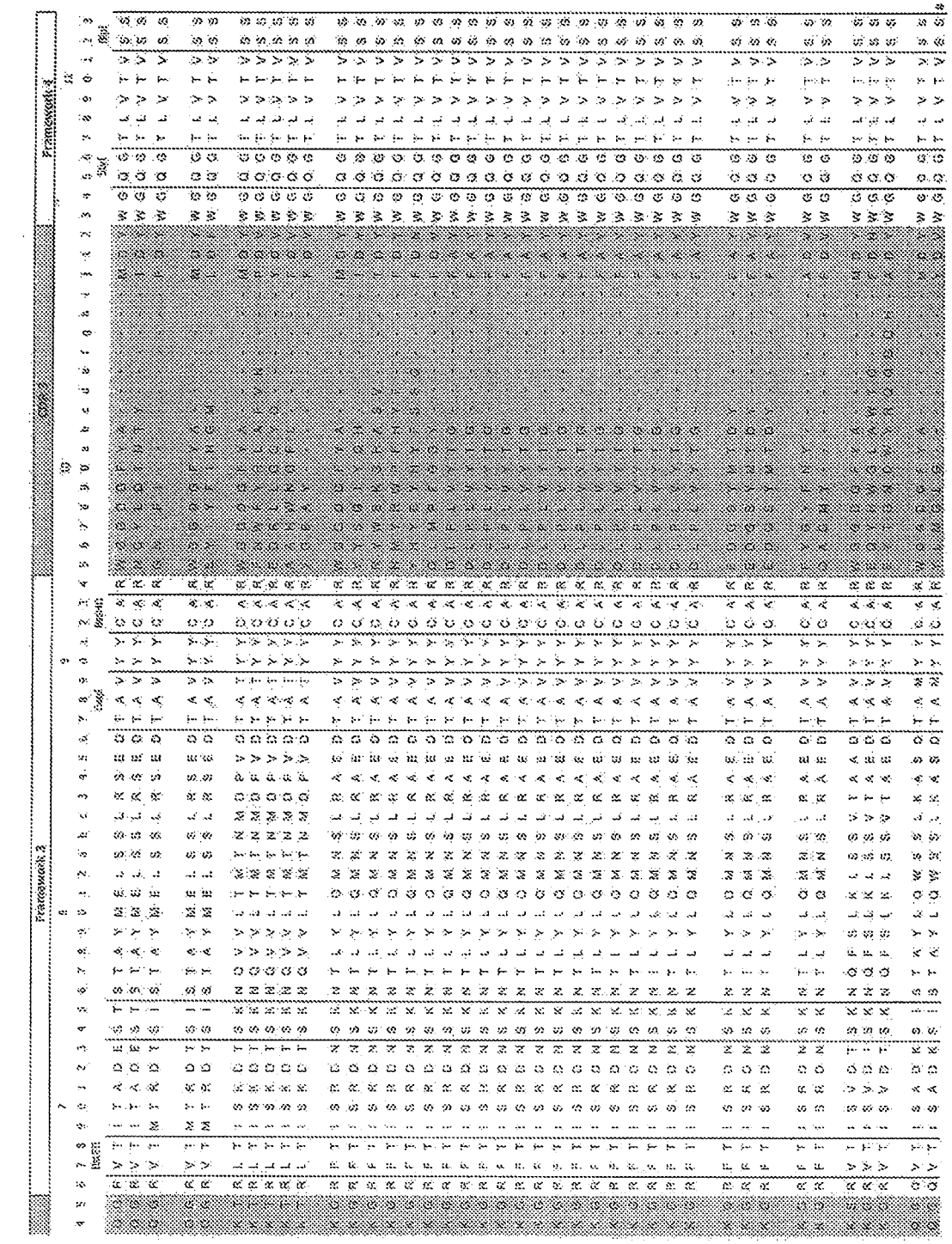

VH
VH sequences CD38 binders
Framework 1
CDR 1
Framework 2
CDR 2
Position
MfeI
BspEI
BstXI
XbaI
VH1A
3076
3085
VH1B
3077
VH2
3086
3101
3128
3131
VH3
3078
3079
3080
3081
3088
3087
6183
6184
6185
6186
6187
6188
6189
6190
6192
6195
6197
6200
6201
3088
6204
6214
3108
3129
VH4
3132
3130
VH5
3127

Figure 14a (Continued)



# Figure 14b

## VL

VL sequences CD38 binders

Restriction sites marked: EcoRV (pos. 1–2), SexAI (pos. 15–16 in λ), BbsI / PstI (pos. 21–23), KpnI (pos. 35–36), XmaI / SexAI (pos. 39–40), BbsI / AseI (pos. 43–47), BsiW I / SanDI (pos. 57–60), BamHI (pos. 7–8 in κ)

| Position | Framework 1 (1–23) | CDR 1 (24–34) | Framework 2 (35–49) | CDR 2 (50–56) | (57–66) |
|---|---|---|---|---|---|
| VLλ1 | DIVLTQPP-SVSGAPGQRVTISC | SGSSSNIGS-----NYVS | WYQQLPGTAPKLLIY | DNNQRPS | GVPDRFS |
| 3085 | DIVLTQPP-SVSGAPGQRVTISC | SGSSSNIGN-----NYVS | WYQQLPGTAPKLLIY | DDDQRPS | GVPDRFS |
| VLλ2 | DIALTQPA-SVSGSPGQSITISC | TGTSSDVGGY----NYVS | WYQQHPGKAPKLMIY | DVSNRPS | GVSNRFS |
| 3076 | DIALTQPA-SVSGSPGQSITISC | TGTSSDIG------AYVS | WYQQHPGKAPKLMIY | EVSSRPS | GVSNRFS |
| 3107 | DIALTQPA-SVSGSPGQSITISC | TSTSSDVGAL----NYVS | WYQQHPGKAPKLMIY | DVNKRPS | GVPDRFS |
| VLλ3 | DIELTQPP-SVSVAPGQTARISC | SGDALGD-------KYAS | WYQQKPGQAPVLVIY | DDSDRPS | GIPERFS |
| 3078 | DIELTQPP-SVSVAPGQTARISC | SGDNIGH-------YYVS | WYQQKPGQAPVLVIY | GDNNRPS | GIPERFS |
| 3080 | DIELTQPP-SVSVAPGQTARISC | SGDNIGN-------SYVS | WYQQKPGQAPVVVIY | DDKNRPS | GIPERFS |
| 3087 | DIELTQPP-SVSVAPGQTARISC | SGDKLGH-------YYVY | WYQQKPGQAPVLVIY | GDSKRPS | GIPERFS |
| 3088 | DIELTQPP-SVSVAPGQTARISC | SGDNIGH-------YYVS | WYQQKPGQAPVLVIY | EDSNRPS | GIPERFS |
| 6278 | DIELTQPP-SVSVAPGQTARISC | SGDNIGH-------YSVS | WYQQKPGQAPVLVIY | SDSNRPS | GIPERFS |
| 6279 | DIELTQPP-SVSVAPGQTARISC | SGDNIGH-------YYVS | WYQQKPGQAPVLVIY | EDSKRPS | GIPERFS |
| 3100 | DIELTQPP-SVSVAPGQTARISC | SGDNIGH-------YYAS | WYQQKPGQAPVLVIY | RDNDRPS | GIPERFS |
| 3101 | DIELTQPP-SVSVAPGQTARISC | SGDSLGS-------YYVH | WYQQKPGQAPVLVIG | DDTKRPS | GIPERFS |
| 3103 | DIELTQPP-SVSVAPGQTARISC | SGDNLGH-------YYVS | WYQQKPGQAPVLVIY | DDSDRPS | GIPERFS |
| 3128 | DIELTQPP-SVSVAPGQTARISC | SGDNIGH-------YYAH | WYQQKPGQAPVVVIY | DDNDRPS | GIPERFS |
| 3129 | DIELTQPP-SVSVAPGQTARISC | SGDKLGS-------KYVS | WYQQKPGQAPVLVIY | YDKKRPS | GIPERFS |
| 3130 | DIELTQPP-SVSVAPGQTARISC | SGDNLGH-------YYVS | WYQQKPGQAPVLVIY | ADNNRPS | GIPERFS |
| 3131 | DIELTQPP-SVSVAPGQTARISC | SGDNLGH-------YYVH | WYQQKPGQAPVLVIY | EDSNRPS | GIPERFS |
| Vκ1 | DIQMTQSPSSLSASVGDRVTITC | RASQSIS-------SYLA | WYQQKPGKAPKLLIY | AASSLQS | GVPSRFS |
| 3079 | DIQMTQSPSSLSASVGDRVTITC | RASQDIS-------AFLN | WYQQKPGKAPKLLIY | KVSNLQS | GVPSRFS |
| 3098 | DIQMTQSPSSLSASVGDRVTITC | RASQNIS-------QWLN | WYQQKPGKAPKLLIY | GASNLQS | GVPSRFS |
| Vκ2 | DIVMTQSPLSLPVTPGEPASISC | RSSQSLLHS-NGYNYLD | WYLQKPGQSPQLLIY | LGSNRAS | GVPDRFS |
| 3077 | DIVMTQSPLSLPVTPGEPASISC | RSSQSLLFL-DGNKYLN | WYLQKPGQSPQLLIY | LGSNRAS | GVPDRFS |
| Vκ3 | DIVLTQSPATLSLSPGERATLSC | RASQSVSS------YLA | WYQQKPGQAPRLLIY | GASSRAT | GVPARFS |
| 3081 | DIVLTQSPATLSLSPGERATLSC | RASQTGSIS-----YLA | WYQQKPGQAPRLLIY | GASKRAT | GVPARFS |
| 3089 | DIVLTQSPATLSLSPGERATLSC | RASQSVSSS-----YLA | WYQQKPGQAPRLLIY | GASSRAT | GVPARFS |

Figure 14b (Continued)

